

TCGACCCACCGTCCGGGAGGATCGGGAGTCGCGGGAGGATGGGCCGCGCTAGGCTCGCACTCCGGA
CGCGCCTCGC
AGTGCAGGGTGGGTGCCCGCCCTGCAGCGTCCGCCGGGCGCGCGGGAGGTGGCCGACAG
GCTCCGGGCC
TCGCAGCCTCAGCCCCGGCCAGCGCGCTTCCGACGGCGGCCGCCAGGCCACCCGCC
CGCCCAAGGTCTCTCGCGGGCGGGAGAACGGAAAACCTCCAACCTCCTGAGTTCTAAAGTTCTGTTG
CTTCAGACAA
TGGATGAGCAATCACAAGGAATGCAAGGGCACCTGTTCCCTAGTTCCAACCACAGAAGGCCTTACGA
CCGGATATGG
GCTATAATACATTAGCCAACTTCGAATAGAAAAGAAAATTGGTCGCGGACAATTAGTGAAG
TTTATAGAGCAGCCTGTCTTGGATGGAGTACCAAGTAGCTTAAAAAAAGTGCAGATATTGATTAA
ATGGATGCCA
AAGCACGTGCTGATTGCATCAAAGAAATAGATCTTCTTAAGCAACTCAACCATCCAAATGTAATAAAA
TATTATGCAT
CATTGAAAGATAATGAACTAAACATAGTTGGAACTAGCAGATGCTGGCACCTATCCA
GAATGATCAAGCATTAAAGAAGCAAAAGAGGCTAATTCTGAAAGAACTGTTGGAAAGTATTGTT
CAGCTTGCA
GTGCATTGAAACACATGCATTCTCGAAGAGTCATGCATAGAGATATAAACAGCTAATGTGTTCA
TACAGCCACTG
GGGTGGTAAAACCTGGAGATCTTGGGCTTGGCCGGTTTCAGCTCAAAACACAGCTGCAC
ATTCTTAGTGGTACGCCATTACATGTCTCCAGAGAGAACATGAAAATGGATACAACCTCAAA
TCTGACATCT
GGTCTTGGCTGTCTACTATATGAGATGGCTGCATTACAAAGTCCTTCTATGGTACAAAATGAAT
TTATACTCAC
TGTGTAAGAAGATAGAACAGTGTGACTACCCACCTCTCCTCAGATCACTATTAGAAC
TCCGACAGTTAGTTAATATGTGCATCAACCCAGATCCAGAGAACGACGTCACCTATGTT
GACGTGCAA
AGAGGATGCATGCAGTCAAGCAGCTAAACATGCAAGATCATGAAGAGTGTAAACCAAGTAATT
GAAAGTATT
TGTGCAAAGTCGTACCTSCCATTATGTCTGGGTGTTAAGATTAATATTGAGAGCTAGTGT
GCTCTGAATCCTAACCAAGTTTCATATAAGCTTCATTGTACCAAGTCACCTAAATCACCTCCTGC
AACCCCCAAA
TGACTTTGAAATAACTGAATTGCATGTTAGGAGAGAAAATGAAACATGATGGTTTGAATGGCTAAAG
GTTTATAGAA
TTTCTTACAGTTCTGCTGATAAATTGTGTTAGATAGACTGTCAGTGCCAAATATTGAAAGG
TGCAGCTTGGCACACATCAGAACATAGACTCATACCTGAGAAAAGTATCTGAACATGTGACTTGT
TTTTTAGTAA
TTTATGGACATTGAGATGAACACAATTGTGAACTTTGTGAGATTTTATTTAACGTTGAAGTA
CTAGTTTAG
TTCTTAGCAGAGTAGTTCAAAATATGATTCTTATGATAAATGTAGACACACAAACTATTGAGA
AACATTAGAACCTTAGCTTACATCAGAACATGTAACTATTAAATGTGAAAGATTGGGACAAAAT
GTGAGTCAGA
CACTGAAGAGTTTTGTTGTTAATATTTGATATTCTCTTGCAATTGAAATGGTATAATGA
ATCCATTAA
AAAGTGGTTAAGGATTGTTAGCTGGTGTGATAATAATTAAAGTTGCACATTGCCAAG
GCTTTTTGTTGTTATTGTTGACATTGAAAGAAATATTCTTGAATAACCTTGCAAGTAC
TATATTCAA

FIGURE 1

TTTCTTATAAATTAAAGTGCATTTAACTCATAATTGTACACTATAATATAAGCCTAAGTTTTATT
CATAAGTTT
ATTGAAGTTCTGATCGGTCCCCTTCAGAAATTTTTATATTATTCTTCAAGTTACTTCTTA
TTTATATTGTATGTGCATTTATCCATTAATGTTCATACTTCTGAGAGTATAATACCCTTAAAAA
GATATTGGT
ATACCAATACTTTCTGGATTGAAAACTTTTAAACTTTAAAATTGGGCCACTCTGTATGCA
TATGTTGGT
CTTGTAAAGAGGAAGAAAGGATGTGTGTTACTGTACCTGTGAATGTGATACAGTTACAA
TTTATTTGACAAGGTTGTAATTCTAGAATATGCTTAATAAAATGAAAACGGCCATGACTACAGCCAG
AACTGTTATG
AGATTAACATTCTATTGAGAAGCTTTGAGTAAAGTACTGTATTTGTTCATGAAGATGACTGAGATG
GTAACACTTC
GTGTAGCTTAAGGAAATGGGCAGAATTCTGAAATGCTGTTGCAGATGTGTTCCCTGAA
TGCTTCGTATTAGTGGCGACCAGTTCTCACAGAATTGTGAAGCCTGAAGGCCAAGAGGAAGTCACT
GTTAAAGGAC
TCTGTGCCATCTAACACCTGGATGAATTATCCTGCCAACGTGAAAACCTCATGTTCAAAGAACACT
TCCCTTTAGC
CGATGTAACGTGGTTTGTTCATATGTGTTTCTTACACTCATTGAATGCTTCAA
GCATTGTAAACTAAAAAAANWAWAAGGGCAAAAGTCTGAACCTGTTCTGAAATCTAATC
AGTTATGTAT
GGTTTCTGAAGGGTAATTTATTTGGAATAGGTAAAGCGAAACCTGTTGTCWTGTTTCCCTGAG
GGCTAGATGC
ATTTTTTCTCACACTCTTAATGACTTTAACATTACTGAGCATCCATAGATATATTCC
TAGAAGTATGAGAAGAATTATTCTTATTGACCATTATGTCATGTTCATTTAATGTAATATAATTGA
GATGAAATGT
TCTCTGGTGGAACAGATACTCTCTTTCTTGCAATCTTAAGAATACTAGATCTAAATTC
ATTAGCTTGA
CCCCTCAAAGTAACTTAAGTAAAGATTAAAGCTTTCTCAGTGAATATATCTGCTAGA
AGGAAATAGCTGGGAAGAATTAAATGATCAGGGAAATTCTTATATGTTGGAAACTTTTGCT
TCGAATATTG
TATCTTTAAATCTAAATGTCATATTTCTGAAGAACCACTGTGAAAAATCAAATTTAATT
TTGAATGGAA
TAATTCAAAGAACTATGAAGATGATTGAGCTCTAATTTATATAGTCACCTATAAAATGTT
CTTTATATGTGTTCATAGTAAATTATATTGATTAAGTAAACTTTGAATTGATTGAGGAGCAG
TAAATGAAA
GCTATATCTATTNCTAAACCYTATTAGACATTGGKACCAGTTACCCAGGTGAAAATAKGGAGTAAC
TTGTTTGTA
TGGTAAGGTTAGGAATGGNGGATGAAGGGTATCTCTATATAAATAAGTGCCTAACATGTG
CAATGATTGTAATTTAGTAAGATATTACAGCCATTGATGCTTACCAACATAGTATCT
ATTACAAAAC
ACCTTCTTGTATCCATATACTCAGGTGTTGCTGTTAACATTACTATGATATTATTTAACCAAA
ATGTTACTCA
CATTAAATGTTATTCTTAAATGAATGATTATGTTAACCCACAAATGCATACTTACC
CTGTGCCTCATATTCAATAGTACTGTAATATGGACATCTTGTGAAATACCTTATTTGTTATGC
TTTAAATATA
CATACAAAAGATTCTGTTATTAGCTTTGAAAATTGTATAATATCCTAATATAACAAAATATAAA
AATAAAAATG
AATACAGTAAAAAAAAAAAAAAAGG

FIGURE 1 (cont'd)

MDEQSQQGMQGPPVQFQPQKALRPDMGYNTLANFRIEKKIGRGQFSEVYRAACLLDGVPA
LKVKVQIF
DLMDAKARAD
CIKEIDLLKQLNHPNVIKYASFIEDNELNIVLELADAGDLSRMIKHFKKQKRLI
PERTVWKFVQLC
SALEHMHSRR
VMHRDIK PANV FIT ATGVVKLGD LGLGRFFSSKTTAAHSLVGT PYYMS PERI HENGYNFKSDI
WSLGCLLYEMAALQSPFYGDKMNL YSLCKKIEQCDY PPLPSDHYSEELRQLVNMCINPDPEKRPDV
TY
VYDVAKRMHA
CTASS

FIGURE 1 (cont'd)

GTGACCCACCGTCCGGTGGAAAGTATAACTTTGTCATTATGAGATGTCGTCTCTCGG
TGCCCTCTTGTGCAAATTAAATTGATGACTGCAGTTTTGAAAACGCGGTGGAGG
AAGTTTGGGAGTGTATCGAGCAAATGGATATCACAGGACAAGGAGGTGGCTGTAAA
GAAGCTCCTCAAAATAGAGAAAGAGGCAGAAACTACAGTCAGTCAGTCACAGAACAT
CATCCAGTTTATGGAGTAATTCTGAAACCTCCAACATGGCATTGTACAGAACATGC
TTCTCTGGGATCACTCTATGATTACATTAAACAGTAACAGAACATGGAGATGGATATGGA
TCACATTATGACCTGGGCCACTGATGAGCCAAAGGAATGCATTATTTACATATGGAGGC
TCCTGTCAAGGTGATTACAGAGACCTCAAGTCAAGAACGTTAGCTGCTGATGG
AGTACTGAAGATCTGTGACTTTGGTGCCTCTCGGTTCCATAAATACACACACATGTC
CTTGGTTGGAACCTTCCCATTGGATGGCTCCAGAAGTTATCCAGAGTCAGTCAGTCAGA
AACTTGTGACACATATTCTATGGTGTGGTTCTCTGGGAGATGCTAACAAAGGGAGGTCCC
CTTAAAGGTTGGAAGGATTACAAGTAGCTTGGCTGTAGTGGAAAAAAACGAGAGATT
AACCATTCCAAGCAGTTGCCAGAAGTTTGCTGAACCTGTTACATCAGTGTGGAGGC
TGATGCCAAGAAACGGCCATATTCAAGCAAATCATTCAATCCTGGAGTCAGTCAGA
TGACACGAGCCTCCTGACAAGTGTAACTCATTCTACACAACAAGGCGGAGTGGAGGTG
CGAAATTGAGGCAACTCTTGAGAGGCTAAAGAAACTAGAGCGTGTAGCTTAAAGGA
GCAGGAGCTTAAAGAACGAGAAAGACGTTAAAGATGTGGGAGCAGACTGACAGAGCA
GTCCAACACCCCGCTCTTGCCTTGTGCAAGAACATGTCTGAGGAGTCTTACATTGA
ATCTAAAACAGAGGAGTCACACAGTCAGAGATGTCAATGTCAGATCACAGCAACAGTAA
CGGGGAGGGCCATGGCATGAACCCAAAGTCTGCAGGCCATGATGCTGATGGCTTGGG
TATCTCTCAATGAACAAAGCAGGAGCTGTGATGCATTCTGGGATGCAGATAAACATGCA
AGCCAAGCAGAATTCTCCAAAACCACATCTAACAGAGAACGGGAGAACAGTCAACATGGC
TCTGGGTTCACTGATTTGACTTGTCAAGAGTGAAGGAGCTGATGATGATGACGGTGA
GGAGGAGGATAATGACATGGATAATAGTGAATGAAAGCAGAAAGCAAAGTAATAAAATCA
CAAATGTTGGAAAACACAAAAGTAACCTGTTATCTCAGTGTACAAAAACAGTAAGG
AGGCAGAAAGCCAAGCACTGCATTAGGCCATCACATTACATGACCGTAATTCTT
ATCAATTCTACTTTATTTGCTTACAGAAAAACGGGGGAGAACATGCAAAGAAGT
ATATTTATGAATCAGCAAATGTGGTGCCTGATTATAGAAATTGTGATCCTATATAAAT
ATAGGACTTTAAAGTTGTGACATTCTGGCTTTCTTTAATGAATACTTTAGTTG
TATTTGACTTATTCTTTATTCAAATCATTAAACTTACATTGAAACAAACAC
TCTTAACTCCTAATTGTTCTTGACACGTAGTAATTCTGTGACATACTTTTTCTTA
TAGCAATAACTGTAATATCAGAAATGGTTGCCCTGAGCAACCTAGTAAGACCTCGTCTC
TACTAATAATTAAAAACTAGCTGGCATGGTAGCACACACCTGTAGTCCCAGATACTGG
GAGGCCAAGGCAGGAGGATTGCTTGAGACCTAGCAATCAGTCAGGGCTGCAGTGAGCCAT
GATGGCACCACTGCACTCTAGCCTGGCAAGAGAACAGATCCTGTCTCAAAAACAAAA
AAAAAAAGGGCGGCCG

MSSLGASFVQIKFDDLQFFENGGGSFGSVYRAKWISQDKEAVK
KLLKIEKEAEILSVLSHRNIIQFYGVILEPPNYGIVTEYASLGSLYDYINSNRSEEMMD
HIMTWAIDVAKGMHYLHEAPVKVIHDLKSRNVIAADGVLKICDFGASRFHNHTTHMS
LVGTPFWMAPEVITQSLPVSETCDTYSYGVVLWEMLTREVPFKLJEGLQVAMLVVERNL
TIPSSCPRSFAELLHQCWEDAKKRPSFKQIISILESMSNDTSLPDKCNSFLHINKAEWRC
EIEATLERLKKLERDLSPKEQELKERERRLKMWEQKLTEQSNTPLLLPLAARMSEESYFE
SKTEESNSAEMSCQITATSNEGHGMNPSLQAMMLMGFGDIFSMNKAGAVMHSGMQLINMQ
AKQNSSKTTSKRRGKKVNMALGFSDFDLSEGDDDDDGEEEDNDMDNSE

FIGURE 2

CGGTGGTGGCGGAGCGGGGCTGCAGGGGGCACCAGGGCCGGGCCACCATGGCCGTGC
GACAGGGCGCTGGGCCGCGGCCTGCAGCTGGTCAGCGCTGCTGCTGCGCTTCACGGCA
AGCCCGGCCGGGCTACGGCTTGGGCGGCCGGGCCGGCGGGCTGTGTCGGCGGG
AGCGTCAGGCTGGCCGAGGACGGGCCGGAGGCCCGAGGGCTGGCCGGCTCG
CTAACCGTGTCCGCTTCCGCCAGTCGGTGGCCGGCTGGCCGGCGGGTTGCAGCGGC
AGTCGTGGTGGCCCTGGGCTGCGGGCCCTGCGCCGGAGTCAGTCTTCTGGCCT
TCGGGCTAGGGCTGGCCTCATCGAGGAAAAACAGCGGAGAGCCGGCGGGCTCG
CCTGTCAAGGAGATCCAGGCAATTTCACCCAGAAAAGCAAGCCGGGCTGACCCGTG
ACACGAGAGGCTTGCAAGGGCTTCGGCTGGAGGAGTATCTGATAGGGCAGTCCATTGTA
AGGGCTGAGTGCCTGCTGTATGAAGCCACCATGCGCTACATTGCCCCAGAACCTGGAGG
TGACAAAGAGCACCGGGTTGCTTCAGGGAGAGGCCAGGTACAGTGCACCAGGAGAAG
GGCAGGGAGCGAGCTCCGGGGCCCTGCGCTCCCTGGCATCAAGATGATGTGAAACA
TCTCGGAGGTCTCCAGCGAAGGCCATCTGAAACACAATGAGGCCAGGAGCTGGTCCCAG
CGAGCCAGTGGCCTTGGCTGGGAGTATGGAGCAGTCACCTACAGAAAATCCAAGAGAG
GTCCCAAGCAACTAGCCCTCACCCCAACATCATCCGGTTCTCGCGCCTTCACCTCTT
CCGTGCGCTGCTGCCAGGGGCCCTGGTCGACTACCCGTATGTCGCCCCACGCCCTCC
ACCCCTGAAGGCCTGGGCATGCCGGACGCTGTTCCCTGTTATGAAGAACTATCCCTGTA
CCCTGCGCCAGTACCTTGTGTAACACACCCAGCCCCGCCTGCCGCATGATGCTGC
TGCAGCTGCTGGAAGGCGTGGACCATCTGGTCAACAGGGCATCGGCACAGAGACCTGA
AATCCGACAACATCCTTGTGGAGCTGGACCCAGACGGCTGCCCTGGCTGGTATCGCAG
ATTTTGGCTGCTGCCCTGGCTGATGAGAGACATCGGCCCTGCAAGTGGCCCTTCAGCAGCTGGT
ACGTGGATCGGGCGGAAACGGCTGCTGATGGCCCCAGAGGTGTCACGCCCGTCC
GCCCGAGGGCAGTGAATTGACTACAGCAAGGCTGATGCCCTGGCAGTGGAGGCCATGCC
ATGAAATCTTCGGGCTTGTCAATCCCTACGCCAGGGCAAGGCCACCTTGAAAGCC
GCAGCTACCAAGAGGCTCAGCTACCTGCACTGCCAGTCAGTGCCTCCAGACGTGAGAC
AGTTGGTGAGGGCACTGCTCCAGCGAGAGGCCAGCAAGAGACCATCTGCCAGTAGCCG
CAAATGTGCTCATCTAACGCTCTGGGTGAACATATTCTAGCCCTGAAGAATCTGAAGT
TAGACAAGATGGTTGGCTGGCTCCTCCAACAATGCCGCCACTTGTGGCAACAGGC
TCACAGAGAAGTGTGTTGGAAACAAAATGAAGATGCTCTTCTGGCTAACCTGGAGT
GTGAAACGCTCTGCCAGGCAGCCCTCCCTCTGCTCATGGAGGGCAGCCCTGTGATGTC
CCTGCATGGAGCTGGTGAATTACTAAAAGAACTTGGCATCCTCTGTGTCGTGATGGTCTG
TGAATGGTGGAGGCTGGAGTCAGGAGACAAGACAGCGCAGAGAGGGCTGGTTAGCCGGAA
AAGGCCTCGGGCTTGGCAAATGGAAAGAACCTGAGTGGAGTTCACTGTCAGTCTG
TCACAGACATCTGAAAGTGAATGGCAAGCTGGTCTAGTAGATGAGGCTGGACTGAGGA
GGGGTAGGCCTGCATCCACAGAGAGGATCCAGGCCAGGCAGTGGCTGTCAGTGGCAGAG
TTTGGCTGTGACCTTGGCCCTAACACGAGGAACCTGTTGAAGGGGGCAGCGTAGCATG
TCTGATTGCCCACCTGGATGAAGGCAGACATCAACATGGGTCAAGCACGTTCAAGTTACGGG
AGTGGGAAATTACATGAGGCCCTGGCTCTGCGTTCCAAGCTGTGCGTTCTGGACCAAGC
TACTGAATTATTAATCTCACTTAGCGAAAGTGAACGGATGAGCAAGTAAGTAAGTGTG
GGGATTAAACTTGAGGGTTTCCCTCTGACTAGCCCTCTTACAGGAATTGTGAAATAT
TAAATGCAAATTACAACGTGCAAAAAAAAAAAAAAAAGGGCGGCC

FIGURE 3

Met Ala

Val Arg Gln Ala Leu Gly Arg Gly Leu Gln Leu Gly Arg Ala Leu Leu
5 10 15

Leu Arg Phe Thr Gly Lys Pro Gly Arg Ala Tyr Gly Leu Gly Arg Pro
20 25 30

Gly Pro Ala Ala Gly Cys Val Arg Gly Glu Arg Pro Gly Trp Ala Ala
35 40 45 50

Gly Pro Gly Ala Glu Pro Arg Arg Val Gly Leu Gly Leu Pro Asn Arg
55 60 65

Leu Arg Phe Phe Arg Gln Ser Val Ala Gly Leu Ala Ala Arg Leu Gln
70 75 80

Arg Gln Phe Val Val Arg Ala Trp Gly Cys Ala Gly Pro Cys Gly Arg
85 90 95

Ala Val Phe Leu Ala Phe Gly Leu Gly Leu Gly Ile Glu Glu Lys
100 105 110

Gln Ala Glu Ser Arg Arg Ala Val Ser Ala Cys Gln Glu Ile Gln Ala
115 120 125 130

Ile Phe Thr Gln Lys Ser Lys Pro Gly Pro Asp Pro Leu Asp Thr Arg
135 140 145

Arg Leu Gln Gly Phe Arg Leu Glu Glu Tyr Leu Ile Gly Gln Ser Ile
150 155 160

Gly Lys Gly Cys Ser Ala Ala Val Tyr Glu Ala Thr Met Pro Thr Leu
165 170 175

Pro Gln Asn Leu Glu Val Thr Lys Ser Thr Gly Leu Leu Pro Gly Arg
180 185 190

Gly Pro Gly Thr Ser Ala Pro Gly Glu Gly Gln Glu Arg Ala Pro Gly
195 200 205 210

Ala Pro Ala Phe Pro Leu Ala Ile Lys Met Met Trp Asn Ile Ser Ala
215 220 225

FIGURE 3 (cont'd)

Gly Ser Ser Ser Glu Ala Ile Leu Asn Thr Met Ser Gln Glu Leu Val
230 235 240

Pro Ala Ser Arg Val Ala Leu Ala Gly Glu Tyr Gly Ala Val Thr Tyr
245 250 255

Arg Lys Ser Lys Arg Gly Pro Lys Gln Leu Ala Pro His Pro Asn Ile
260 265 270

Ile Arg Val Leu Arg Ala Phe Thr Ser Ser Val Pro Leu Leu Pro Gly
275 280 285 290

Ala Leu Val Asp Tyr Pro Asp Val Leu Pro Ser Arg Leu His Pro Glu
295 300 305

Gly Leu Gly His Gly Arg Thr Leu Phe Leu Val Met Lys Asn Tyr Pro
310 315 320

Cys Thr Leu Arg Gln Tyr Leu Cys Val Asn Thr Pro Ser Pro Arg Leu
325 330 335

Ala Ala Met Met Leu Leu Gln Leu Leu Glu Gly Val Asp His Leu Val
340 345 350

Gln Gln Gly Ile Ala His Arg Asp Leu Lys Ser Asp Asn Ile Leu Val
355 360 365 370

Glu Leu Asp Pro Asp Gly Cys Pro Trp Leu Val Ile Ala Asp Phe Gly
375 380 385

Cys Cys Leu Ala Asp Glu Ser Ile Gly Leu Gln Leu Pro Phe Ser Ser
390 395 400

Trp Tyr Val Asp Arg Gly Gly Asn Gly Cys Leu Met Ala Pro Glu Val
405 410 415

Ser Thr Ala Arg Pro Gly Pro Arg Ala Val Ile Asp Tyr Ser Lys Ala
420 425 430

FIGURE 3 (cont'd)

Asp Ala Trp Ala Val Gly Ala Ile Ala Tyr Glu Ile Phe Gly Leu Val
435 440 445 450

Asn Pro Phe Tyr Gly Gln Gly Lys Ala His Leu Glu Ser Arg Ser Tyr
455 460 465

Gln Glu Ala Gln Leu Pro Ala Leu Pro Glu Ser Val Pro Pro Asp Val
470 475 480

Arg Gln Leu Val Arg Ala Leu Leu Gln Arg Glu Ala Ser Lys Arg Pro
485 490 495

Ser Ala Arg Val Ala Ala Asn Val Leu His Leu Ser Leu Trp Gly Glu
500 505 510

His Ile Leu Ala Leu Lys Asn Leu Lys Leu Asp Lys Met Val Gly Trp
515 520 525 530

Leu Leu Gln Gln Ser Ala Ala Thr Leu Leu Ala Asn Arg Leu Thr Glu
535 540 545

Lys Cys Cys Val Glu Thr Lys Met Lys Met Leu Phe Leu Ala Asn Leu
550 555 560

Glu Cys Glu Thr Leu Cys Gln Ala Ala Leu Leu Leu Cys Ser Trp Arg
565 570 575

Ala Ala Leu

FIGURE 3 (cont'd)

GTCGACCCACGCGGTCCGCCACCGCGTCCGGAGACATGTCTGTGTTTC
TCTCCCTCCGCTTTGAGTCCGTTGAAGACACAATTCTCTGTGGGGT
GCTTAGGAGGAGCTCATGAACATGTATTGAATTGGACTAGCTGAACAG
GCTGCTGGTGGCTGCCAGAGGGGGCAGGCTGTGTTGCTGGAGCCTC
CAGCTCCCTGCAGCAGTCATGGGCAGGGTCCCCGAGTCCGTAATCCCC
ATTCCACCTACTTCCCTAGTTATTGATTCCCTGTCTGTCGTACTCAGC
TTAAGTGGAGCATCCCTTCTGGAGACACGAAGCAGGAAACACTGGC
AAATATCACAGCAGTGAGTTACGACTTGTATGAGGAATTCTCAGCCAGA
CGAGCGAGCTGCCAAGGACTTATTGGAAAGCTCTGGTAAAGAGACC
CGGAAACGGCTACAATCCAAGAGGCTCTCAGACACCCCTGGATCACGCC
GGTGGACAACCAGCAAGCCATGGTGCAGGGAGTCTGTGGTCAATCTGG
AGAACTTCAGGAAGCAGTATGTCCGCAGGCGGTGGAAGCTTCCTCAGC
ATCGTGTCCCTGTGCAACCACCTCACCCGCTCGTGATGAAGAAGGTGCA
CCTGAGGCCGGATGAGGACCTGAGGAACCTGTGAGAGTGACACTGAGGAG
GACATGCCAGGAGGAAAGCCCTCACCCACGGAGGAGGAGCACACCT
CCTAAGTGGCTGACCTGCAGTGGCCGCCAGGGAGGTCTGGGCCAGCGG
GGCTCCCTCTGTGCAAGACTTGGACCCAGCTCAGCACCAGCACCCGGGC
GTCCTGAGCACTTGCAAGAGAGATGGGCCAACCGAATTCAAAGAGCTT
GCAGGCAAGCCAGGAGACCCCTGGGAGCTGTGGCTGTCTGTGGAGGAG
GCTCCAGCATTCCCAAAGCTCTAATTCTCCATAAAATGGCTTCCCTCTG
TCTGCCATCCTCAGAGTCTGGGTGGAGTGTGGACTTAGGAAAACAATA
TAAAGGACATCCTCATCATCACGGGTTGAAGGTCAAGACTAACGGCAGCCTT
CTTCACAGGCTGAGGGGGTTCAGAACCCAGCTGGCCAAAAATTACACCAAG
AGAGACAGAGTCCTCCCCATTGGGAACAGGGTATTGAGGAAAGTGAACC
TTGGGTGTGAGGGACCAATCCTGTGACCTCCCAGAACCATGGAAGGCCAGG
ACGTCAAGGCTGACCAACACCTCAGACCTCTGAAGCAGCCCATTGCTGGC
CCGCCATGTTGTAATTGCTCATTTATTAAACTCTGGTTACCTGATG
CTTGGCTCTTTAGGGCTACCCCATCTCATTCTTAGCCCAGTGCCT
GTAACTCTGAGGGGGGCACCCAGTGGGTGCTGAGTGGCAGAACATCTCA
GAAGGTCTCCTGAACCGTCCGCGAGGCCTGCAGTGGCCTGCCTCCTC
CTTGCTTCCCTAACAGGAAGGTGTCAGTCAAGAGAACCCACCCAGAGA
CTGGGAGTGGTGGCTACGCCTATAATCCCTGCCTTGGCAGTCCGAGG
CAGGGGAATTGCTGAACTCAGGAGTGGAGACCAGCCTGGCAACATGG
AAAAACGCAGTCTGTACAAAAAAATACAAAAAAATTAGCCAGGTGAGGGT
AGGCACCTGGCATCCCAGCTACTCCAGGGCTGAGGTGACAGCATTGCTT
AAGCCCAGAAGGTGAGGCTGCAGTGAGCTGAGATCACGCCACTGCACTC
CAGTCTGGGTGACAGAGAGAGACCATATCCAAAAAAAGGG
CGGCCGC

LFDSLGVLSLSGASPFLGDTKQETLANITA VSYDFDEEFFSQTSELAKDFIRKL
LVKETRKRLTIQEALRHPWITPVDNQQAMVRRESVNLENFRKQYVRRRWK
LSFSIVSLCNHLTRSLMKVHLRPDEDLRNCESDTEEDIARRKALHPRRRSSTS

FIGURE 4

T A L A K E L R E L R I E E T N R P N	19
G ACG GCA TTA GCG AAA GAA CTA AGA GAA CTC CGG ATT GAA GAA ACA AAC CGC CCA ATG	57
K K V T D Y S S S B E S E S S E E E E	39
AAG AAG GTG ACT GAT TAC TCC TCC AGT GAG GAG TCA GAA AGT AGC GAG GAA GAG GAG	117
E D G E S E T H D G T V A V S D I P R L	59
GAA GAT CGA GAG AGC GAG ACC CAT GAT GGG ACA GTG GCT GTC AGC GAC ATA CCC AGA CTG	177
I P T G A P G S N E Q Y N V G H V G T H	79
ATA CCA ACA CGA GCT CCA CGC ACC AAC GAG CAG TAC AAT GTG GGA ATG GTG GGG ACG CAT	237
G L E T S H A D S P S G S I S R E G T L	99
GGG CTG GAG ACC TCT CAT CGG GAC AGT TTC AGC CGC AGT ATT TCA AGA GAA GGA ACC TTG	297
M I R E T S G E K K R S G H S D S N G F	119
ATG ATT AGA GAG ACG TCT CGA GAG AAG CGA TCT CGC CAC AGT GAC AGC AAT GGC TTT	357
A G H I N L P D L V Q Q S H S P A G T P	139
GCT CGC CAC ATC AAC CTC CCT GAC CTG GTG CAG CAG ACC CAT TCT CCA GCT GGA ACC CGG	417
T E G L G R V S T H S Q E M D S G T E Y	159
ACT GAG GGA CTG GGG CGC GTC TCA ACC CAT TCC CAG GAG ATG GAC TCT GGG ACT GAA TAT	477
G A G S S T K A S F T P F V D P R V Y Q	179
GCG ATG GGG AGC ACC AAA GCC TCC TTC ACC CCC TTT GTG GAC CGC AGA GTA TAC CAG	537
T S P T D E D E E D E S S A A A A L F T	199
ACG TCT CCC ACT GAT GAA GAT GAA GAG GAT GAG GAA TCA TCA GCG GCA GCT CTG TTT ACT	597
S E L L R Q E Q A K L N E A R K I S V V	219
AGC GAA CTT CTT AGG CAA GAA CAG CGC AAA CTC AAT GAA GCA AGA AAG ATT TCG GTG GTA	657
N V N P T N I R P H S D T P E I R K Y K	239
AAT GTA AAC CGA ACC AAC ATT CGG CCT CAT AGC GAC ACA CGA GAA ATC AGA AAA TAC AAG	717
K R F N S E I L C A A L W G V N L L V G	259
AAA CGA TTC AAC TCA GAA ATA CTT TGT GCA GCT CTG TGG GGT GTA AAC CTT CTG GTG GGG	777
T E N G L M L L D R S G Q G K V Y N L I	279
ACT GAA AAT CGC CTG ATG CTT TTG GAC CGA AGT GGG CAA CGC AAA GTC TAT ATT CTG ATC	837
N R R R F Q Q M D V L E G L N V L V T I	299
AAC CGG AGG CGA TTT CAG CAG ATG GAT GTG CTA GAG GGA CTG AAT GTC CTT GTG ACA ATT	897
S G K K N K L R V Y Y L S W L R N R I L	319
TCA CGA AAG AAG AAT AAG CTA CGA GTT TAC TAT CTT TCA TGG TTA AGA AAC AGA ATA CTA	957
H N D P E V E K K Q G W I T V G D L E G	339
CAT AAT GAC CGA GAA GTA GAA AAG AAA CAA CGC TGG ATC ACT GTT GGG GAC TTG GAA CGC	1017
C I H Y K V V K Y E R I K F L V I A L K	359
TGT ATA CAT TAT AAA GTT GTT AAA TAT GAA AGG ATC AAA TTT TTG GTG ATT GCC TTA AAG	1077
N A V E I Y A W A P K P Y H K F M A F K	379
AAT GCT GTG GAA ATA TAT GCT TGG GCT CCT AAA CGG TAT CAT AAA TTC ATG GCA TTT AAG	1137
S F A D L Q H K P L L V D L T V E E G Q	399
TCT TTT GCA GAT CTC CAG CAC AAG CCT CTG CTA GTT GAT CTC ACG GTA GAA GAA GGT CAA	1197
R L K V I F G S H T G F H V I D V D S C	419

FIGURE 5

AGA TTA AAG GTT ATT TTT GGT TCA CAC ACT GGT TTC CAT GTC ATT GAT GTT GAT TCA GGA 1257
N S Y D I Y I P S H I Q G N I T P H A I 439
AAC TCT TAT GAT ATC TAC ATA CCA TCT CAT ATT CAG GGC AAT ATC ACT CCT CAT GCT ATT 1317
V I L P K 444
GTC ATC TTG CCT AAA 1332

FIGURE 5 (cont'd)